

Serial No. 09/311,689
Group Art Unit: 1652

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1-8. (Cancelled)

9. (Previously Presented) A polypeptide with at least 30% sequence identity to the polypeptide of Seq. ID No. 2 and comprising greater than fifty amino acids in length and modified in order to have a composition selected from one of the following: at least 5-15 mole % methionine, at least 6-25 mole % threonine, and at least 4-9 mole % tryptophan; wherein the % sequence identity is based on the entire sequence and is determined by BLAST 2.0 using default parameters.

10. (Previously Presented) A polypeptide comprising Seq. ID No. 2 or 4 modified to contain seven or more non-native essential amino acid residues at positions corresponding to the positions in Seq. ID No. 2 selected from 1, 8, 11, 17, 18, 19, 20, 22, 23, 31, 34, 38, 40, 41, 47, 49, 56, 58, 59, 60, 61, 62, 63, 65, 67, 69, 73, 75, 76, 78, 79, 81, 82 or combinations thereof; and further provided that the polypeptide has at least 30% sequence identity to the polypeptide of Seq. ID No. 2 or 4, wherein the percent identity is determined by Blast 2.0 using default parameters.

11. (Previously Presented) The polypeptide of Claim 10 wherein the essential amino acid residues comprise isoleucine, lysine, threonine, tryptophan, methionine, leucine, valine or combinations thereof hereof.

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12. (Previously Presented) The polypeptide of Claim 10 wherein the protein exhibits reduced inhibitory activity against chymotrypsin, subtilisin or elastase when compared with the inhibitory activity against chymotrypsin, subtilisin or elastase exhibited by Seq. ID No. 4.
13. (Currently Amended) The polypeptide of claim 10 wherein the polypeptide further comprises one or more of the following modifications: V32T[(:)] , E45T[(:)] , D64T[(:)] , D74T[(:)] , or A77T.
14. (Currently Amended) The polypeptide of claim 10, further comprising one of the following pairs of substitutions: T22C and V82C[(:)] or E23C and R81C.
15. (Original) The polypeptide of Claim 10 further comprising an amino-terminal extension.
16. (Previously Presented) The polypeptide according to claim 15 wherein the amino terminal extension comprises essential amino acids.
17. (Previously Presented) The polypeptide of Claim 15 wherein the amino-terminal extension is a methionine or a transit peptide.
18. (Previously Presented) The polypeptide of Claim 15 wherein the amino-terminal extension comprises at least one to eighteen additional residues corresponding to amino acid residues 1 to 18 of Seq. ID No. 2 or 12.
19. (Previously Presented) A polypeptide comprising Seq. ID No. 2 modified to contain two or more modifications, said two or more modifications corresponding to positions in Seq. ID No. 2 selected from the group consisting of:

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H18A, H18I, H18L, H18V, H18M, N19K, N19T, L20M, L20I, L20V, E23T, E23K, S31T, S32K, E34K, E34T, V38M, V38I, V38L, L40M, L40I, L40V, Q41K, Q41T, Q47K, Q47T, I49M, I49I, I49L, I49V, I56K, I56T, M59G, R62K, R62T, I63M, I63L, I63V, R65K, R65T, R67K, R67T, F69W, L73K, L73T, N75K, N75T, Q78K, Q78T, V79T, V79K, R81K, and R81T; and

further provided that the polypeptide is a nutritional supplement and has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters.

20. (Currently Amended) The polypeptide according to claim 19 wherein the modifications further comprise one or more of the following pairs of substitutions: E23C and R81C[[:]] , T22C and V82C[[:]] , or V53C and V70C.

21. (Previously Presented) A polypeptide comprising Seq. ID No. 2 modified to contain two or more modifications, said two or more modifications corresponding to positions in Seq. ID No. 2 selected from the group consisting of:

H18A, H18M, N19K, L20M, T22C, E23T, E23C, S31T, E34K, V38M, L40M, Q41K, Q47K, I49M, I56K, M59G, R62K, I63M, R65K, R67K, F69W, L73K, N75K, Q78K, V79T, R81K, R81C, and V82C; and

further provided that the polypeptide is a nutritional supplement and has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters.

22. (Previously Presented) The polypeptide of claim 21, further comprising substituting a tryptophan at position 61.

23. (Original) The polypeptide of claim 22, further comprising threonine at one or more of positions 32, 45, 53, 64 or 70.

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24. (Currently Amended) The polypeptide of claim 22 wherein the modifications comprise one or more of the following pairs of substitutions: E23C and R81C[[:]] or T22C and V82C.

25. (Original) The polypeptide according to claim 22 further comprising an insert in the active site loop region that is enriched in essential amino acids for the purpose of nutritional enhancement.

26-27. (Cancelled)

28. (Previously Presented) A polypeptide comprising Seq. ID No. 2 modified to contain three or more modifications, said three or more modifications comprising non-native essential amino acids replacing native amino acids at positions corresponding to Seq. ID No. 2 and selected from the group consisting of positions 1, 8, 11, 17, 18, 19, 20, 22, 23, 31, 32, 34, 38, 40, 41, 45, 47, 49, 56, 58, 59, 60, 61, 62, 63, 64, 65, 67, 69, 73, 74, 75, 76, 77, 78, 79, 81 and 82; and excluding V and W at position 56; K, V and W at position 58; W, V and K at position 59; T, I and K at position 60; V and W at position 61 and V and F at position 62; and

further provided that the polypeptide is a nutritional supplement and has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters.

29. (Previously Presented) An isolated polypeptide comprising Seq. ID No. 6, 8, 10, 12, 14, 16, 18, 20 or a conservatively substituted polypeptide thereof, wherein said isolated polypeptide or conservatively substituted polypeptide thereof has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters.

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30. (Previously Presented) An isolated polypeptide comprising at least twenty three contiguous amino acids of Seq. ID Nos. 6, 8, 10, 12, 14, 16, 18 or 20, wherein said isolated polypeptide or conservative substitution thereof has at least 30% sequence identity to the polypeptide of Seq. ID No. 2, wherein the percent identity is determined by Blast 2.0 using default parameters.

31. (Previously Presented) An isolated polypeptide with more than 79% sequence identity to the polypeptide of Seq. ID No. 20, wherein the percent sequence identity is determined by GAP analysis using Gap Weight of 12 and Length Weight of 4.

32-53. (Cancelled)

54. (Previously Presented) The polypeptide of claim 9, wherein the polypeptide is modified in order to have a composition of at least 5-15 mole % methionine.

55. (Previously Presented) The polypeptide of claim 9, wherein the polypeptide is modified in order to have a composition of at least 6-25 mole % threonine.

56. (Previously Presented) The polypeptide of claim 10 wherein the non-native essential amino acid residues comprise lysine and the positions correspond to the positions in Seq. ID No. 2 selected from 1, 8, 11, 17, 19, 34, 41, 56, 59, 62, 65, 67, 73 or combinations thereof.

57. (Original) Food or feed comprising the polypeptide of claim 30.

58. (Original) Food or feed comprising the polypeptide of claim 31.

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59. (Previously Presented) An isolated polypeptide with at least 60% sequence identity to the polypeptide of Seq. ID No. 2 comprising greater than fifty amino acids in length and comprising more than ten lysine amino acid residues.

60. (Cancelled)

61. (Previously Presented) An isolated polypeptide comprising Seq. ID Nos. 6, 8, 10, 12, 14, 16, 18 or 20.

62. (Cancelled)

63. (Previously Presented) The polypeptide of claim 72, wherein the non-native essential amino acids are isoleucine, lysine, tryptophan, methionine, threonine, or mixtures thereof.

64. (Previously Presented) The polypeptide of claim 72, wherein the non-native essential amino acids are lysine.

65. (Previously Presented) The polypeptide of claim 72, further comprising an amino terminal extension.

66. (Previously Presented) The polypeptide of claim 65, wherein the amino terminal extension comprises a methionine.

67. (Original) The polypeptide of claim 65, wherein the amino terminal extension comprises essential amino acids.

68. (Cancelled)

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69. (Previously Presented) The polypeptide of claim 72, wherein the non-native di-sulfide bond is with a non-native cysteine at one or more positions corresponding to Seq. ID No. 4 positions 23, 81, 22, 82, 53 or 70.

70. (Previously Presented) The polypeptide of claim 72, further comprising at least two non-native cysteines.

71. (Currently Amended) The polypeptide of claim 70, wherein the non-native cysteines are at one or more of the following pairs of positions: T22C and V82C[[:]] or E23C and R81C.

72. (Previously Presented) A polypeptide comprising Seq. ID No. 4, wherein said polypeptide has been modified to contain at least one non-native disulfide bond and more than four non-native essential amino, and wherein said modified polypeptide has at least 30% sequence identity to the polypeptide of Seq. ID No. 4, the percent sequence identity determined by Blast 2.0 using default parameters.

73-75. (Cancelled)

76. (Previously Presented) A polypeptide comprising Seq. ID No. 4, wherein said polypeptide has been modified to contain at least eleven non-native essential amino acids, and wherein said modified polypeptide has at least 30% sequence identity to the polypeptide of Seq. ID No. 4, the percent sequence identity determined by Blast 2.0 using default parameters.

77. (Original) The polypeptide of claim 76 wherein the non-native essential amino acids are lysine.

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78. (Previously Presented) A polypeptide having at least 80% sequence identity to the polypeptide of Seq. ID No. 2 and modified to contain a non-native disulfide bond.

79. (Previously Presented) A polypeptide having at least 80% identity to the polypeptide of Seq. ID No. 6 and modified to contain a non-native disulfide bond.

80. (Previously Presented) The polypeptide of claim 79, having at least 90% sequence identity to the polypeptide of Seq. ID No. 6.

81. (Previously Presented) A polypeptide having at least 80% sequence identity to the polypeptide of Seq. ID No. 8 and modified to contain a non-native disulfide bond.

82. (Previously Presented) The polypeptide of claim 81, having at least 90% sequence identity to the polypeptide of Seq. ID No. 8.

83. (Previously Presented) A polypeptide having at least 80% sequence identity to the polypeptide of Seq. ID No. 10 and modified to comprise a non-native disulfide bond.

84. (Previously Presented) The polypeptide of claim 83, having at least 90% sequence identity to the polypeptide of Seq. ID No. 10.

85. (Previously Presented) The polypeptide of claim 84, wherein the non-native disulfide bond is formed with a cysteine residue at one or more of positions 23, 81, 22, 82, 53 or 70.

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86. (Currently Amended) The polypeptide of claim 85, wherein the non-native disulfide bond is formed between cysteine residues substituted at one or more of the following pairs of positions: 22 and 82[[:]] or 23 and 81.

87. (Previously Presented) A polypeptide comprising any one of Seq. ID Nos. 35-53, wherein the polypeptide is modified to have a non-native disulfide bond and more than seven non-native essential amino acid residues, wherein said polypeptide has at least 30% sequence identity to the polypeptide of Seq. ID No. 2 as determined by Blast 2.0 using default parameters.

88-95. (Cancelled)

96. (Original) The polypeptide of claim 10 further comprising the pair of substitutions that is V53C and V70C.

97. (Original) The polypeptide of claim 22, further comprising the pair of substitutions that is V53C and V70C.

98-99. (Cancelled)